



1	ATG	GCT	GGA	CCT	GCC	ACC	CAG	AGC	CCC	ATG	AAG	CTG	ATG	GCC	CTG	45
46	CAG	CTG	CTG	TGG	TGG	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	90
91	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	135
136	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	GCG	CTC	180
181	CAG	GAG	AAG	CTG	GCA	GGC	TGC	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	225
226	TTC	CTC	TAC	CAG	GGG	CTC	CTG	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	270
271	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA	CTG	CAG	CTG	GAC	GTC	GCC	GAC	315
316	TTT	GCC	ACC	ATC	ATC	TGG	CAG	CAG	ATG	GAA	GAA	CTG	GGA	ATG	GCC	360
361	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	405
406	GCT	TTC	CAG	CGC	CGG	GCA	GGA	GGG	GTC	CTA	GTT	GCC	TCC	CAT	CTG	450
451	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC	CGC	GTT	CTA	CGC	CAC	CTT	GCC	495
496	CAG	CCC	TAA	TAA												508

(see: SEQ ID NO: 17)

stop codon

FIG. 1

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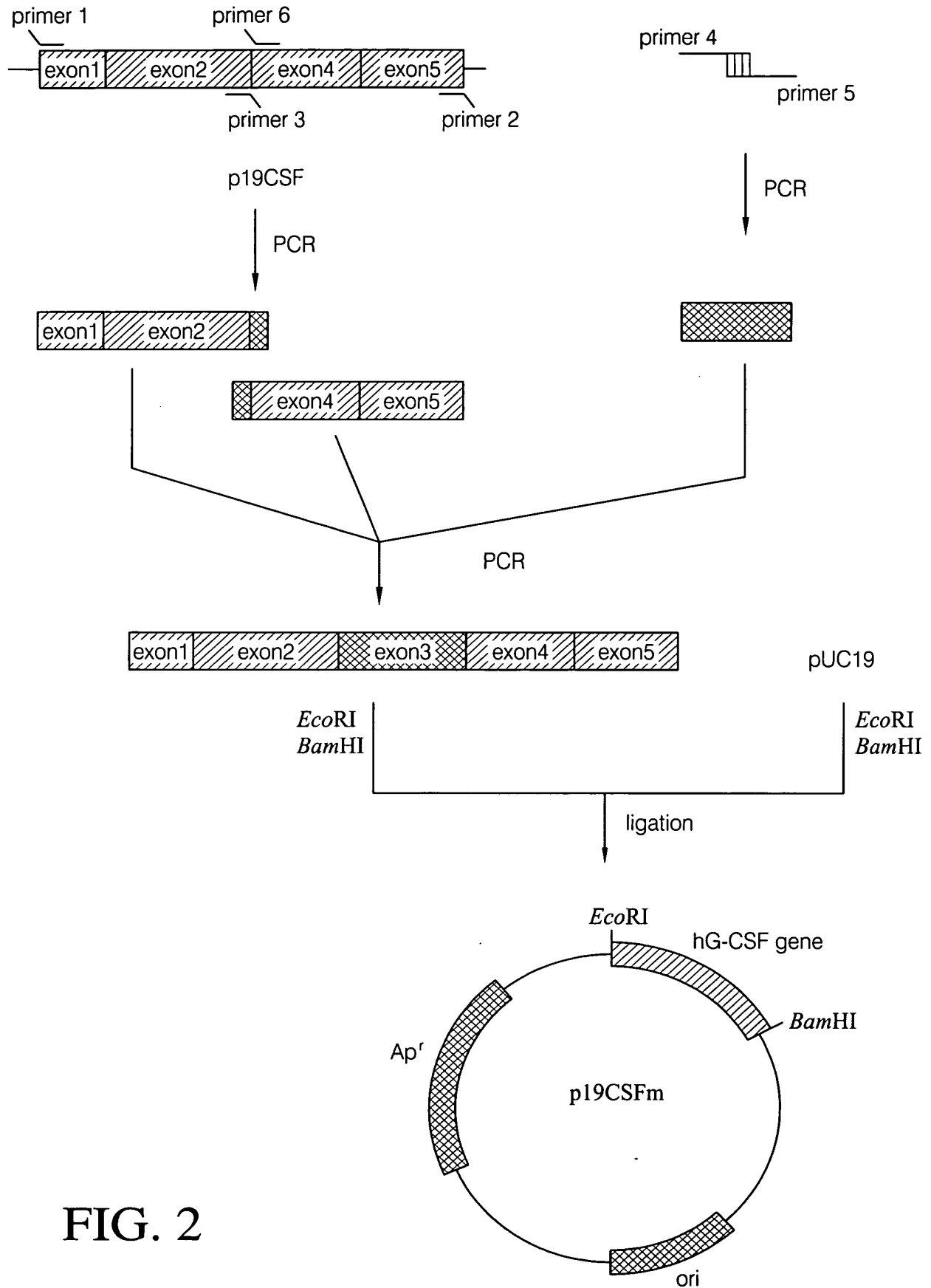


FIG. 2

ESCHERICHIA COLI STRAIN SECRETING HUMAN GRANULOCYTE...

Sang-Yup Lee

Appl. No.: 10/009,792 Atty Docket: HYLEE60.001APC

Replacement Sheet

3/13																
-30															-16	
1	ATG	GCT	GGA	CCT	GCC	ACC	CAG	AGC	CCC	ATG	AAG	CTG	ATG	GCC	CTG	45
-15															-1	+1
46	CAG	CTG	CTG	CTG	TGG	AGT	GCA	CTC	TGG	ACA	GTG	CAG	GAA	GCC	ACC	90
															Thr	
2															16	
91	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	CTC	AAG	135
	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	Leu	Lys	
17															31	
136	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	GCG	CTC	180
	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	Ala	Leu	
32															46	
181	CAG	GAG	AAG	CTG	TGT	GCC	ACC	TAC	AAG	CTG	TGC	CAC	CCC	GAG	GAG	225
	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	Glu	Glu	
47															61	
226	CTG	GTG	CTG	CTC	GGA	CAC	TCT	CTG	GGC	ATC	CCC	TGG	GCT	CCC	CTG	270
	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	Pro	Leu	
62															76	
271	AGC	AGC	TGC	CCC	AGC	CAG	GCC	CTG	CAG	CTG	GCA	GGC	TGC	TTG	AGC	315
	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	Leu	Ser	
77															91	
316	CAA	CTC	CAT	AGC	GGC	CTT	TTC	CTC	TAC	CAG	GGG	CTC	CTG	CAG	GCC	360
	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	Gln	Ala	
92															106	
361	CTG	GAA	GGG	ATC	TCC	CCC	GAG	TTG	GGT	CCC	ACC	TTG	GAC	ACA	CTG	405
	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	Thr	Leu	
107															121	
406	CAG	CTG	GAC	GTC	GCC	GAC	TTT	GCC	ACC	ACC	ATC	TGG	CAG	CAG	ATG	450
	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	Gln	Met	
122															136	
451	GAA	GAA	CTG	GGA	ATG	GCC	CCT	GCC	CTG	CAG	CCC	ACC	CAG	GGT	GCC	495
	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	Gly	Ala	
137															151	
496	ATG	CCG	GCC	TTC	GCC	TCT	GCT	TTC	CAG	CGC	CGG	GCA	GGA	GGG	GTC	540
	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	Gly	Val	
152															166	
541	CTA	GTT	GCC	TCC	CAT	CTG	CAG	AGC	TTC	CTG	GAG	GTG	TCG	TAC	CGC	585
	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	Tyr	Arg	
167															174	
586	GTT	CTA	CGC	CAC	CTT	GCC	CAG	CCC	TAA	TAA						616
	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	stop	codon						

(see: SEQ ID NO: 18)

(see: SEQ ID NO: 19)

FIG. 3

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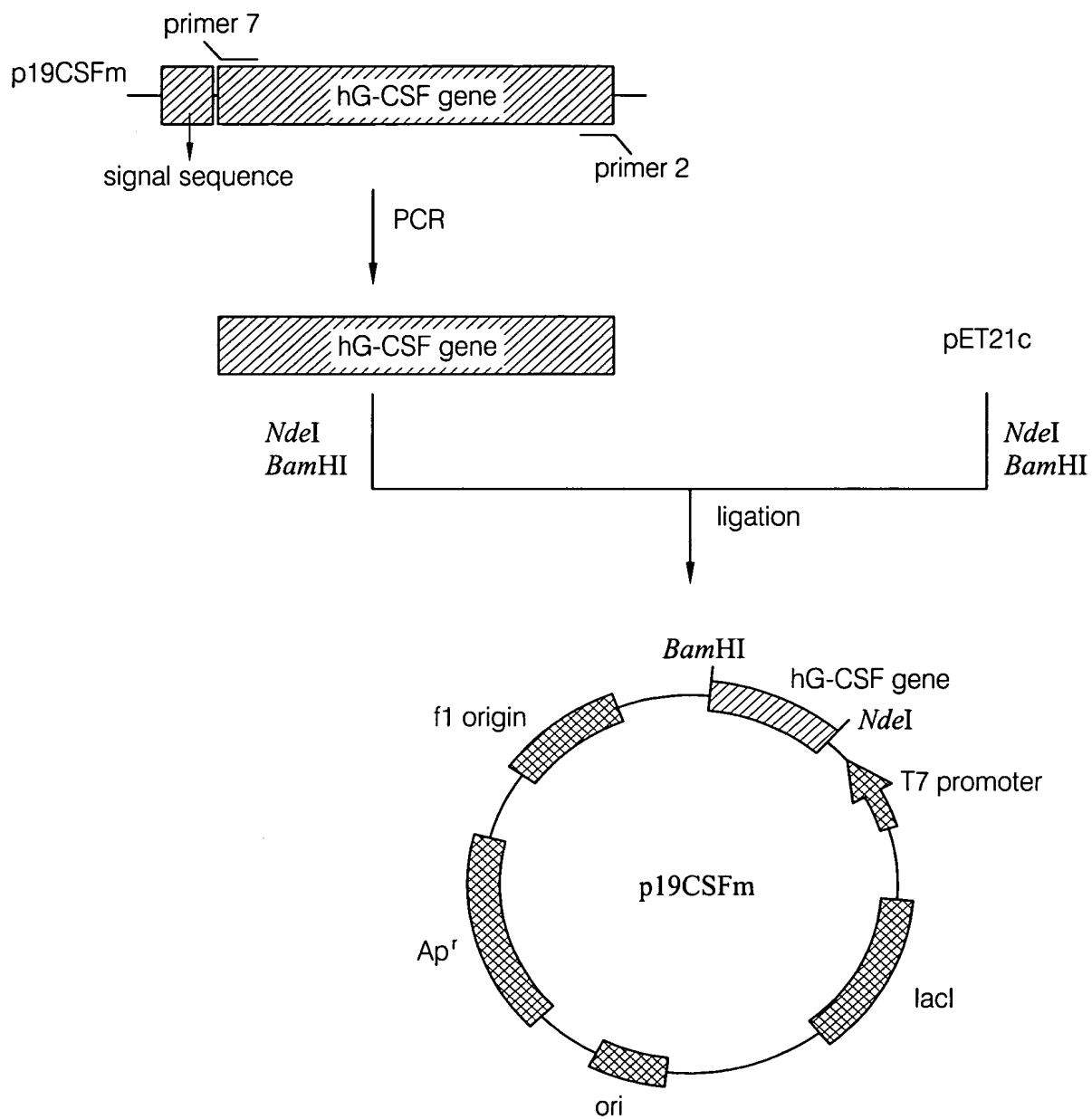


FIG. 4

ESCHERICHIA COLI STRAIN SECRETING HUMAN GRANULOCYTE...

Sang-Yup Lee

Appl. No.: 10/009,792 Atty Docket: HYLEE60.001APC

Replacement Sheet

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1	ATG	ACC	CCC	CTG	GGC	CCT	GCC	AGC	TCC	CTG	CCC	CAG	AGC	TTC	CTG	15
1	Met	Thr	Pro	Leu	Gly	Pro	Ala	Ser	Ser	Leu	Pro	Gln	Ser	Phe	Leu	45
16																30
46	CTC	AAG	TGC	TTA	GAG	CAA	GTG	AGG	AAG	ATC	CAG	GGC	GAT	GGC	GCA	90
	Leu	Lys	Cys	Leu	Glu	Gln	Val	Arg	Lys	Ile	Gln	Gly	Asp	Gly	Ala	
31																45
91	GCG	CTC	CAG	GAG	AAG	CTG	TGT	GCC	ACC	TAC	AAG	CTG	TGC	CAC	CCC	135
	Ala	Leu	Gln	Glu	Lys	Leu	Cys	Ala	Thr	Tyr	Lys	Leu	Cys	His	Pro	
46																60
136	GAG	GAG	CTG	GTG	CTG	CTC	GGA	CAC	TCT	CTG	GGC	ATC	CCC	TGG	GCT	180
	Glu	Glu	Leu	Val	Leu	Leu	Gly	His	Ser	Leu	Gly	Ile	Pro	Trp	Ala	
61																75
181	CCC	CTG	AGC	AGC	TGC	CCC	AGC	CAG	GCC	CTG	CAG	CTG	GCA	GGC	TGC	225
	Pro	Leu	Ser	Ser	Cys	Pro	Ser	Gln	Ala	Leu	Gln	Leu	Ala	Gly	Cys	
76																90
226	TTG	AGC	CAA	CTC	CAT	AGC	GGC	CTT	TTC	CTC	TAC	CAG	GGG	CTC	CTG	270
	Leu	Ser	Gln	Leu	His	Ser	Gly	Leu	Phe	Leu	Tyr	Gln	Gly	Leu	Leu	
91																105
271	CAG	GCC	CTG	GAA	GGG	ATC	TCC	CCC	GAG	TTG	GGT	CCC	ACC	TTG	GAC	315
	Gln	Ala	Leu	Glu	Gly	Ile	Ser	Pro	Glu	Leu	Gly	Pro	Thr	Leu	Asp	
106																120
316	ACA	CTG	CAG	CTG	GAC	GTC	GCC	GAC	TTT	GCC	ACC	ACC	ATC	TGG	CAG	360
	Thr	Leu	Gln	Leu	Asp	Val	Ala	Asp	Phe	Ala	Thr	Thr	Ile	Trp	Gln	
121																135
361	CAG	ATG	GAA	GAA	CTG	GGA	ATG	GCC	CCT	GCC	CTG	CAG	CCC	ACC	CAG	405
	Gln	Met	Glu	Glu	Leu	Gly	Met	Ala	Pro	Ala	Leu	Gln	Pro	Thr	Gln	
136																150
406	GGT	GCC	ATG	CCG	GCC	TTC	GCC	TCT	GCT	TTC	CAG	CGC	CGG	GCA	GGA	450
	Gly	Ala	Met	Pro	Ala	Phe	Ala	Ser	Ala	Phe	Gln	Arg	Arg	Ala	Gly	
151																165
451	GGG	GTC	CTA	GTT	GCC	TCC	CAT	CTG	CAG	AGC	TTC	CTG	GAG	GTG	TCG	495
	Gly	Val	Leu	Val	Ala	Ser	His	Leu	Gln	Ser	Phe	Leu	Glu	Val	Ser	
166																175
496	TAC	CGC	GTT	CTA	CGC	CAC	CTT	GCC	CAG	CCC	TAA	TAA				531
	Tyr	Arg	Val	Leu	Arg	His	Leu	Ala	Gln	Pro	stop	codon				

(see: SEQ ID NO: 20)

(see: SEQ ID NO: 21)

FIG. 5

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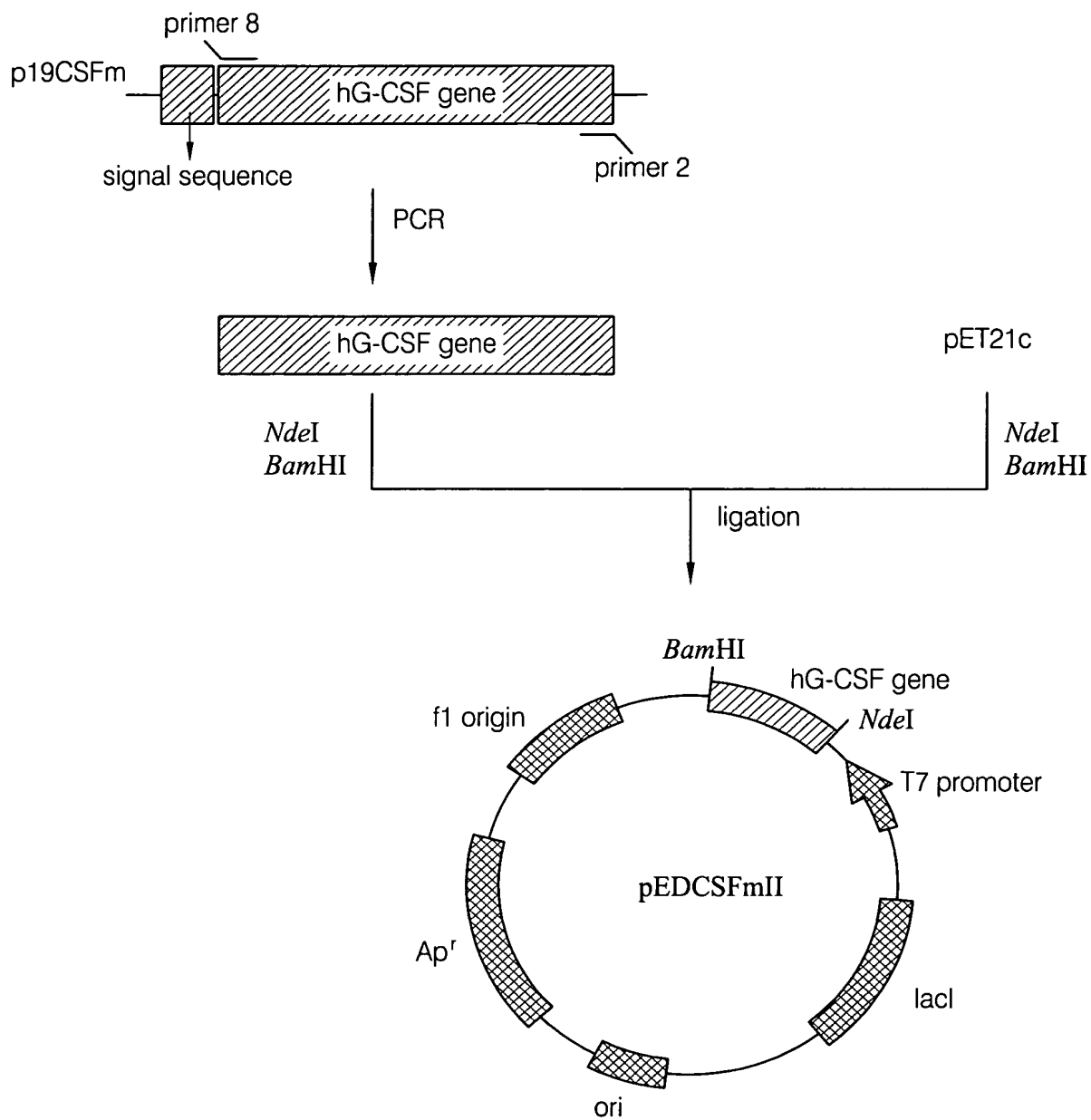


FIG. 6

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1 15 45
1 ATG ACT CCG TTA GGT CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG
Met Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu

(see: SEQ ID NO: 22)

(see: SEQ ID NO: 23)

FIG. 7

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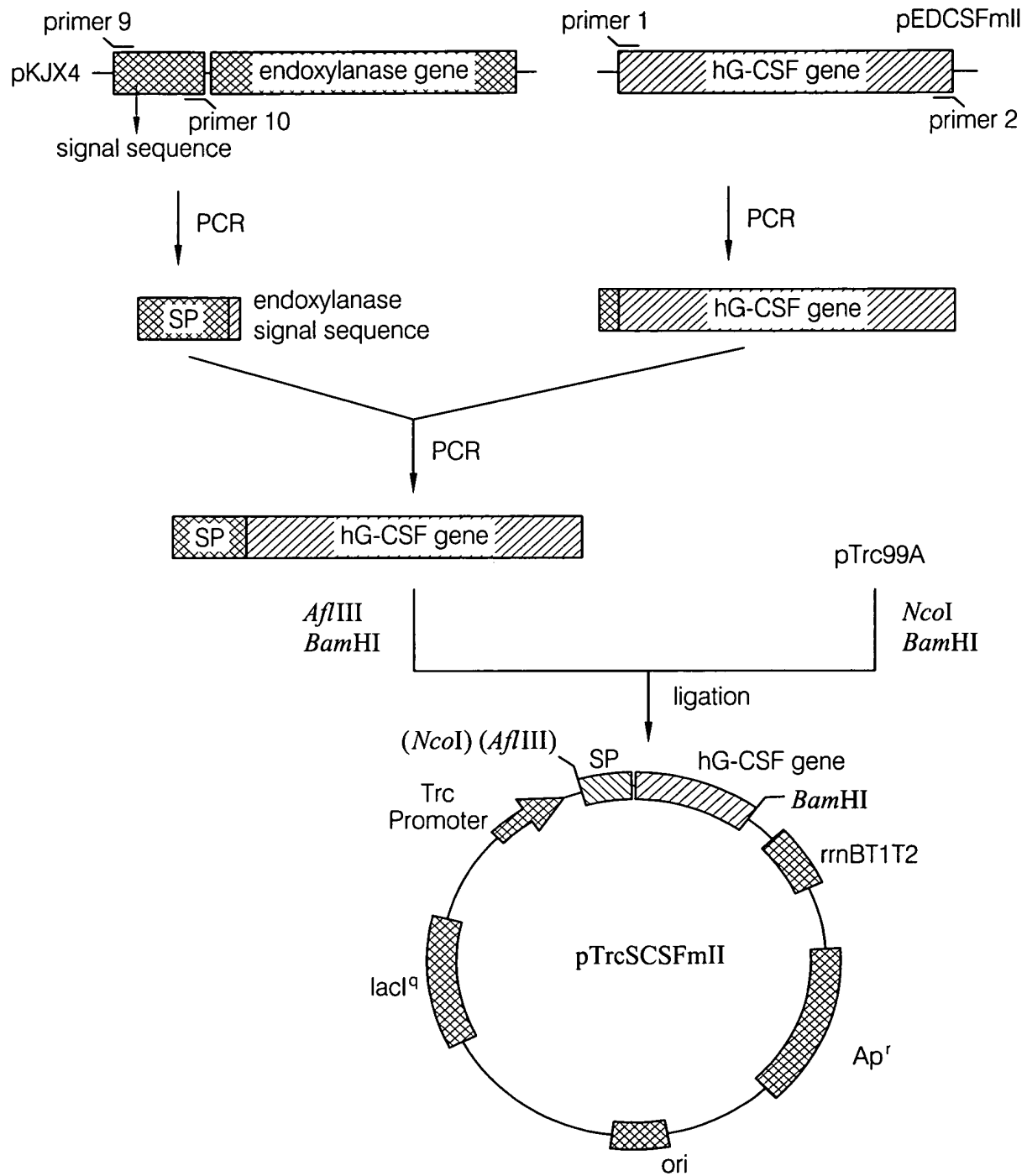


FIG. 8

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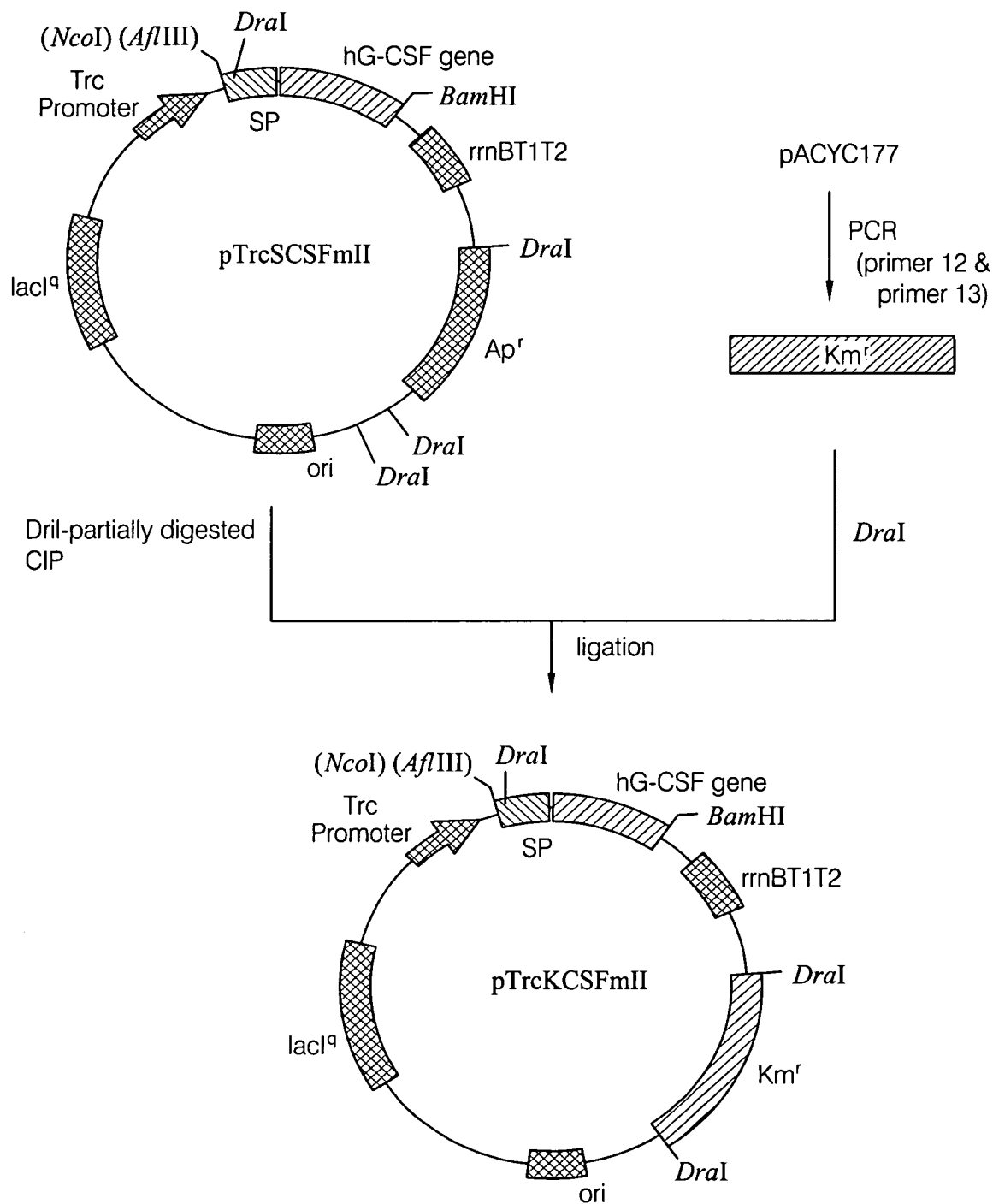


FIG. 10

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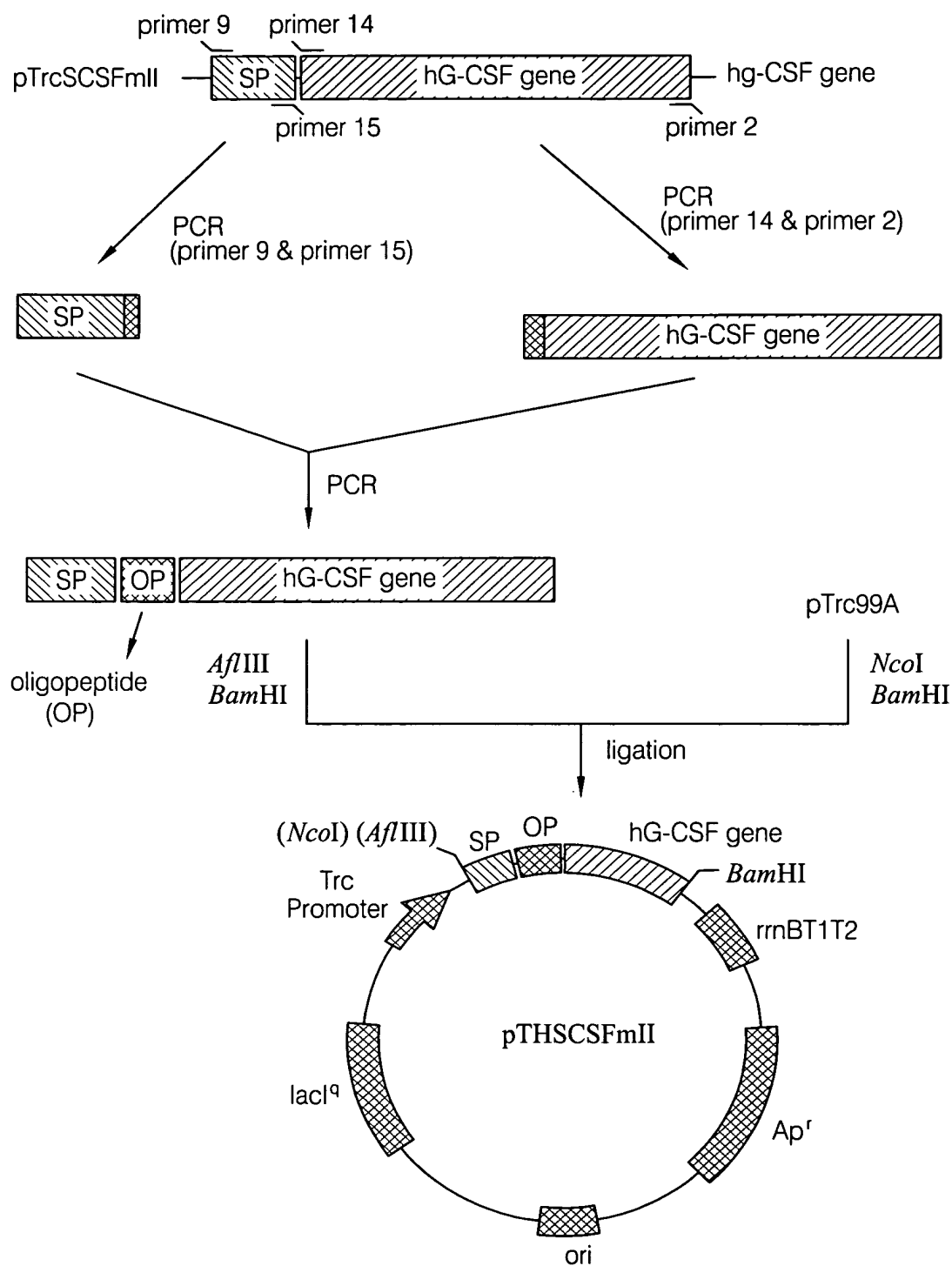


FIG. 11

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-28          -14          45
1  ATG TTT AAG TTT AAA AAG AAA TTC TTA GTG GGA TTA ACG GCA GCT
   Met Phe Lys Phe Lys Lys Lys Phe Leu Val Gly Leu Thr Ala Ala

-13          -1  +1  2
46 TTC ATG AGT ATC AGC ATG TTT TCT GCA ACC GCC TCT GCA GCT GGC 90
   Phe Met Ser Ile Ser Met Phe Ser Ala Thr Ala Ser Ala Ala Gly

3          17
91 CCG CAC CAT CAC CAT CAC CAT ATC GAG GGA AGG ACT CCG TTA GGT 135
   Pro His His His His His His Ile Glu Gly Arg Thr Pro Leu Gly

18          32
136 CCA GCC AGC TCC CTG CCC CAG AGC TTC CTG CTC AAG TGC TTA GAG 180
     Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys Cys Leu Glu

(see: SEQ ID NO: 26)
(see: SEQ ID NO: 27)

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FIG. 12

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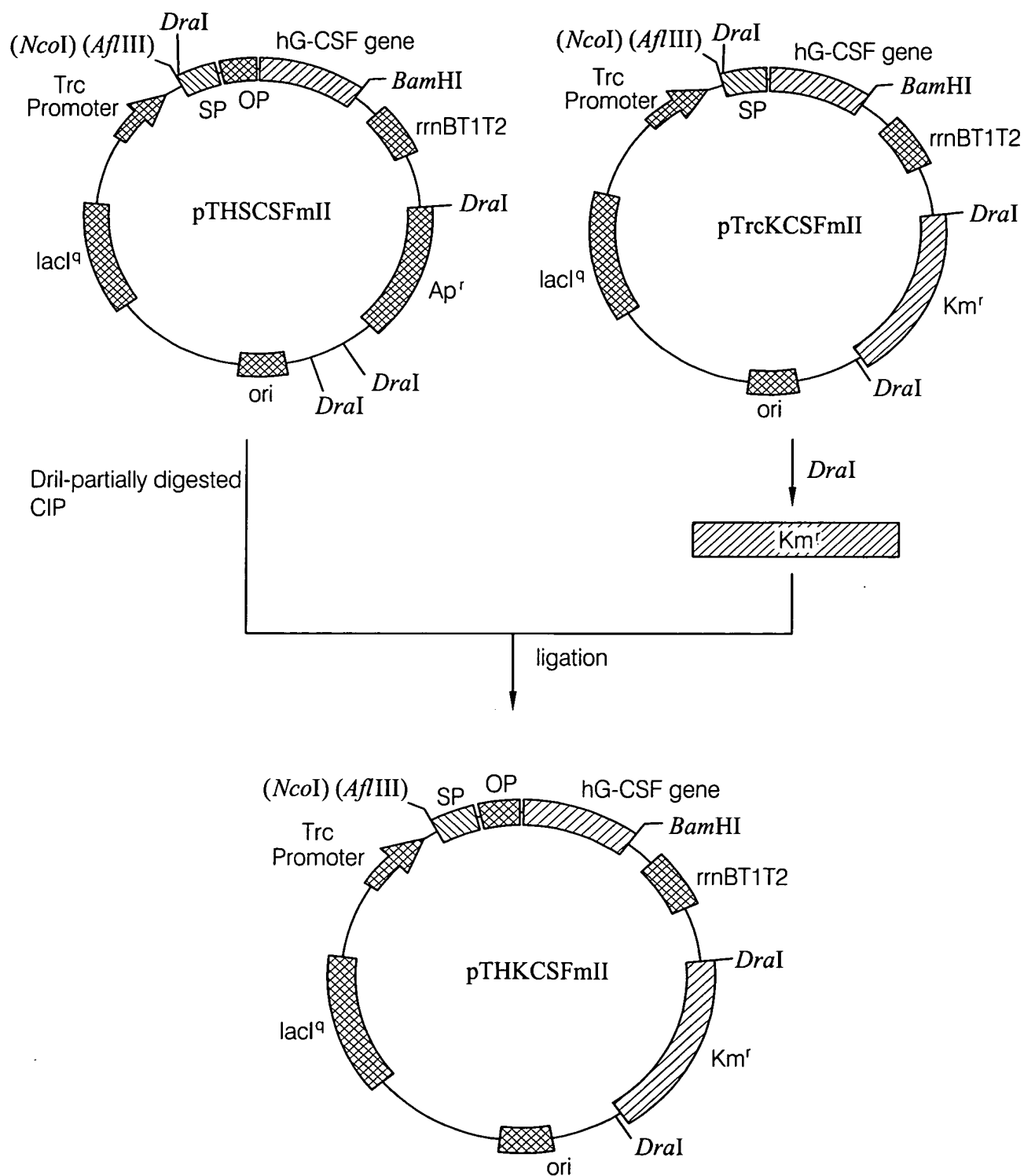


FIG. 13